



## SEQUENCE LISTING

&lt;110&gt; THE SCRIPPS RESEARCH INSTITUTE

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&lt;120&gt; ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR

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&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Xenopus

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(1)

&lt;223&gt; Xaa is Tyr or Phe

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (2)..(2)

&lt;223&gt; Xaa is any Amino Acid

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(7)

&lt;223&gt; Xaa is any Amino Acid

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (9)..(11)

&lt;223&gt; Xaa is any Amino Acid

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (13)..(17)

&lt;223&gt; Xaa is any Amino Acid

F9

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 <222> (19)..(20)  
 <223> Xaa is any Amino Acid

<220>  
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 <222> (22)..(25)  
 <223> Xaa is any Amino Acid

<220>  
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 <222> (27)..(32)  
 <223> Xaa is any Amino Acid

<220>  
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 <222> (6)..(6)  
 <223> Xaa may be missing

<220>  
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 <222> (7)..(7)  
 <223> Xaa may be missing

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 <222> (25)..(25)  
 <223> Xaa may be missing

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 <222> (29)..(29)  
 <223> Xaa may be missing

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 <222> (30)..(30)  
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 <222> (31)..(31)  
 <223> Xaa may be missing

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 <222> (32)..(32)  
 <223> Xaa may be missing

<400> 1

Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa  
 1 5 10 15

Xaa Leu Xaa Xaa His Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30

<210> 2  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for amplification of pZif89

<400> 2  
 atgaaactgc tcgagcccta tgcttgccct gtcgag 36

<210> 3  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for amplification of pZif89

<400> 3  
 gaggaggagg agactagtgt ccttctgtct taaatggatt ttggt 45

<210> 4  
 <211> 273  
 <212> DNA  
 <213> Mouse

<220>  
 <221> CDS  
 <222> (1)..(273)  
 <223>

<400> 4  
 ctc gag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct 48  
 Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser  
 1 5 10 15

cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc cag aag 96  
 Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys  
 20 25 30

ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt gac cac 144  
 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His  
 35 40 45

ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt gcc tgt 192  
 Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys  
 50 55 60

gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag agg cat 240  
 Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His  
 65 70 75 80

acc aaa atc cat tta aga cag aag gac act agt 273  
 Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser  
 85 90

<210> 5

<211> 91  
 <212> PRT  
 <213> Mouse

<400> 5

Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser  
 1 5 10 15

Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys  
 20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His  
 35 40 45

Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys  
 50 55 60

Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His  
 65 70 75 80

Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser  
 85 90

<210> 6  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> FTX3 primer

<400> 6  
 gcaattaacc ctcactaaag gg

22

<210> 7  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> BZF3 primer

<400> 7  
 ggcaaacttc ctcccacaaa t

21

<210> 8  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> ZF36K primer

<220>  
 <221> misc\_feature  
 <222> (22)..(41)  
 <223> n is any nucleotide  
  
 <400> 8  
 atttgtggga ggaagtttgc cnnkagtnnk nnknnknnkn nkcataccaa aatccattta 60  
  
 <210> 9  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> R3B primer  
  
 <400> 9  
 ttgatattca caaacgaatg g 21  
  
 <210> 10  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> ZFNsiB primer  
  
 <400> 10  
 catgcatatt cgacactgga a 21  
  
 <210> 11  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> ZF2r6F primer  
  
 <220>  
 <221> misc\_feature  
 <222> (28)..(44)  
 <223> n is any nucleotide  
  
 <400> 11  
 cagtgtcgaa tatgcatgcg taacttcnnk nnknnknnkn nknnkaccac ccacatccgc 60  
 acccac 66  
  
 <210> 12  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> ZFI6rb primer

<220>  
 <221> misc\_feature  
 <222> (26)..(45)  
 <223> n is any nucleotide

<400> 12  
 ctggcctgtg tggatgcgga tatgmnnmnn mnnmnnmnnnc gamnnagaaa agcggcgatc 60  
 gcagga 66

<210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> ZFIF primer

<400> 13  
 catatccgca tccacacagg ccag 24

<210> 14  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 14

Arg Ser Asp Glu Leu Thr Arg His  
 1 5

<210> 15  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 15

Ser Arg Ser Asp His Leu  
 1 5

<210> 16  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Hairpin oligonucleotide of a phage library containing phages

<400> 16  
 cgtaaattggg cgcccttttg ggcgcccatt tacg 34

<210> 17  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Binding sequence of zif268 finger 3  
 <400> 17

Arg Ser Asp Glu Arg Lys Arg His  
 1 5

<210> 18  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Binding sequence of zif268 finger 3  
 <400> 18

Trp Ser Ile Pro Val Leu Leu His  
 1 5

<210> 19  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Binding sequence of zif268 finger 3  
 <400> 19

Trp Ser Leu Leu Pro Val Leu His  
 1 5

<210> 20  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Binding sequence of zif268 finger 3  
 <400> 20

Phe Ser Phe Leu Leu Pro Leu His  
 1 5

<210> 21  
 <211> 8  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 21

Leu Ser Thr Trp Arg Gly Trp His  
1 5

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 22

Thr Ser Ile Gln Leu Pro Tyr His  
1 5

<210> 23

<211> 61

<212> DNA

<213> Homo sapiens

<400> 23

tgatctcaga agccaagcag ggtcgggcct ggtagtact tggatgggag accgcctggg 60

a 61

<210> 24

<211> 26

<212> PRT

<213> Homo sapiens

<400> 24

Tyr Ile Cys Ser Phe Ala Asp Cys Gly Ala Ala Tyr Asn Lys Asn Trp  
1 5 10 15

Lys Leu Gln Ala His Leu Cys Lys His Thr  
20 25

<210> 25

<211> 26

<212> PRT

<213> Homo sapiens

<400> 25

Phe Pro Cys Lys Glu Glu Gly Cys Glu Lys Gly Phe Thr Ser Leu His  
1 5 10 15



His Leu Thr Arg His Ser Leu Thr His Thr  
 20 25

<210> 26  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens  
 <400> 26

Phe Thr Cys Asp Ser Asp Gly Cys Asp Leu Arg Phe Thr Thr Lys Ala  
 1 5 10 15

Asn Met Lys Lys His Phe Asn Arg Phe His  
 20 25

<210> 27  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 tggatgggag acc

13

<210> 28  
 <211> 25  
 <212> PRT  
 <213> Mouse

<400> 28

Arg Gln Lys Asp Ser Arg Thr Ser Thr Ser Gly Gln Ala Gly Gln Tyr  
 1 5 10 15

Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 20 25

<210> 29  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for amplification of fragments of zif268

<400> 29  
 gtccataaga ttagcggatc c

21

<210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for amplification of fragments of zif268

&lt;400&gt; 30

gtgagcgagg aagcggaaga g

21

&lt;210&gt; 31

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; zif268 consensus binding site

&lt;400&gt; 31

cctgcgtggg cgcccttttg ggcgcccacg cagg

34

&lt;210&gt; 32

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Linker peptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(4)

&lt;223&gt; Xaa is Lys or Pro

&lt;400&gt; 32

Thr Gly Glu Xaa

1

&lt;210&gt; 33

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(459)

&lt;223&gt;

&lt;400&gt; 33

atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc  
 Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg  
 1 5 10 15

48

ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc  
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly  
 20 25 30

96

cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt  
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser  
 35 40 45

144

gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192  
 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe  
 50 55 60

gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240  
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys  
 65 70 75 80

agg cat acc aaa atc cat acc ggt cag aag ccc act agt ggc ggt ggt 288  
 Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly  
 85 90 95

cgg atc gcc cgg ctg gag gaa aaa gtg aaa acc ttg aaa gcg caa aac 336  
 Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn  
 100 105 110

tcc gag ctg gcg tcc acc gcc aac atg ctc agg gaa cag gtg gca cag 384  
 Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln  
 115 120 125

ctt aaa cag aaa gtc atg aac cac gct agc ggc cag gcc ggc cag tac 432  
 Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr  
 130 135 140

ccg tac gac gtt ccg gac tac gct tct taa 462  
 Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 145 150

<210> 34  
 <211> 153  
 <212> PRT  
 <213> Mouse

<400> 34

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg  
 1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly  
 20 25 30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser  
 35 40 45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe  
 50 55 60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys  
 65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly  
 85 90 95

Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn

100	105	110	
Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln			
115	120	125	
Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr			
130	135	140	
Pro Tyr Asp Val Pro Asp Tyr Ala Ser			
145	150		
<210>	35		
<211>	462		
<212>	DNA		
<213>	Mouse		
<220>			
<221>	CDS		
<222>	(1) .. (459)		
<223>			
<400>	35		
atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc			48
Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg			
1 5 10 15			
ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc			96
Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly			
20 25 30			
cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt			144
Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser			
35 40 45			
gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt			192
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe			
50 55 60			
gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag			240
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys			
65 70 75 80			
agg cat acc aaa atc cat acc ggt cag aag ccc act agt ggc ggt ggt			288
Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly			
85 90 95			
ctg acc gac acc ctg cag gcg gaa acc gac cag ctg gaa gac gaa aaa			336
Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys			
100 105 110			
tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag			384
Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys			
115 120 125			
ctg gag ttc atc ctg gcg gca cac gct agc ggc cag gcc ggc cag tac			432
Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr			
130 135 140			

ccg tac gac gtt ccg gac tac gct tct taa  
 Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 145 150

462

<210> 36  
 <211> 153  
 <212> PRT  
 <213> Mouse

<400> 36

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg  
 1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly  
 20 25 30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser  
 35 40 45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe  
 50 55 60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys  
 65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly  
 85 90 95

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys  
 100 105 110

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys  
 115 120 125

Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr  
 130 135 140

Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 145 150

<210> 37  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Single stranded leucine zipper domain of zif268-Jun

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> n is any nucleotide. n can be any number of nucleotides

<400> 37  
 cgccccacgcg gcgtgggcg

19

<210> 38  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Single-stranded leucine zipper domain of zif268-Fos

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> n is any nucleotide. n can be any number of nucleotides

<400> 38  
 cgccccacgcg gcggcgggcg cggcggcg

28

<210> 39  
 <211> 67  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Construction of C7 zinc finger

<220>  
 <221> MISC\_FEATURE  
 <222> (67)..(67)  
 <223> Xaa is Tyr-Ala-Cys-Pro-Val-Glu-Ser-Cys-Asp-Arg-Arg-Phe-Ser-Lys-  
 -Ser-Ala-Asp-Leu-Lys-Arg-His-Ile-Arg-Ile-His-Thr-Gly-Glu-Lys-Pro  
 could be repeated 10 times

<400> 39

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg  
 1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr  
 20 25 30

Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe  
 35 40 45

Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu  
 50 55 60

Lys Pro Xaa  
 65

<210> 40  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide hairpin

<400> 40  
 cctcgccgcc gcgggttttc ccgcgcccc gagg 34

<210> 41  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(294)  
 <223>

<400> 41  
 atg aaa ctg ctc gag ccc tat gct tgc cct gtc gag tcc tgc gat cgc 48  
 Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg  
 1 5 10 15

cgc ttt tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac act 96  
 Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr  
 20 25 30

ggc gaa aaa ccg tac gcg tgc cct gtc gag tcc tgc gat cgc cgc ttt 144  
 Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe  
 35 40 45

tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggg gag 192  
 Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu  
 50 55 60

aag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct aag 240  
 Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys  
 65 70 75 80

tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggt cag aag ccc 288  
 Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro  
 85 90 95

act agt 294  
 Thr Ser

<210> 42  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 42

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg  
1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr  
20 25 30

Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe  
35 40 45

Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu  
50 55 60

Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys  
65 70 75 80

Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro  
85 90 95

Thr Ser

<210> 43  
<211> 543  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> zif268-zif268 with TGEKP linker

<220>  
<221> CDS  
<222> (1)..(543)  
<223>

<400> 43  
atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc 48  
Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg  
1 5 10 15  
  
ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc 96  
Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly  
20 25 30  
  
cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144  
Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser  
35 40 45  
  
gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192  
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe  
50 55 60  
  
gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240  
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys  
65 70 75 80



agg cat acc aaa atc cat acc ggg gag aag ccc tat gct tgc cct gtc 288  
 Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val  
                     85                    90                    95

gag tcc tgc gat cgc cgc ttt tct cgc tcg gat gag ctt acc cgc cat 336  
 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His  
                     100                    105                    110

atc cgc atc cac aca ggc cag aag ccc ttc cag tgt cga ata tcc atg 384  
 Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met  
                     115                    120                    125

cgt aac ttc agt cgt agt gac cac ctt acc acc cac atc cgc acc cac 432  
 Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His  
                     130                    135                    140

aca ggc gag aag cct ttt gcc tgt gac att tgt ggg agg aag ttt gcc 480  
 Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala  
                     145                    150                    155                    160

agg agt gat gaa cgc aag agg cat acc aaa atc cat tta aga cag aag 528  
 Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys  
                     165                    170                    175

gac tct aga act agt 543  
 Asp Ser Arg Thr Ser  
                     180

<210> 44  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> zif268-zif268 with TGEKP linker

<400> 44

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg  
 1                    5                    10                    15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly  
                     20                    25                    30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser  
                     35                    40                    45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe  
                     50                    55                    60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys  
 65                    70                    75                    80

Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val

85

90

95

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His  
 100 105 110

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met  
 115 120 125

Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His  
 130 135 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala  
 145 150 155 160

Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys  
 165 170 175

Asp Ser Arg Thr Ser  
 180

<210> 45  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for generation of 5' C7

<400> 45  
 gaggaggagg agggatccat gctogagctc ccctatgctt gccctg

46

<210> 46  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for generation of 5' C7

<400> 46  
 gaggaggaga ccggtatgga ttttggtatg cctcttgcg

39

<210> 47  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for generation of 3' C7

<400> 47  
 gaggaggaga ccggtgagaa gccctatgct tgccctgtcg agtcctgcga tcgccgc

57

<210> 48  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for generation of 3' C7

<400> 48  
 gaggaggaga ctagttctag agtccttctg tc 32

<210> 49  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primary strand within a duplex region of a probe for C7-C7 site

<400> 49  
 gatgtatgta gcgtgggcgg cgtgggcgta agtaatgc 38

<210> 50  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primary strand within a duplex region of a probe for SP1C-C7 site

<400> 50  
 gatgtatgta gcgtgggcgg gggcggggta agtaatgc 38

<210> 51  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primary strand within a duplex region of a probe for (GCG)<sub>6</sub> site

<400> 51  
 gatgtatgta gcggcggcgg cggcggcgta agtaatgc 38

<210> 52  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primary strand within a duplex region of a probe for C7 site

<400> 52  
 gatgtatgta gcgtgggcgt aagtaatgc 29

<210> 53  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primary strand within a duplex region of a probe for Sp1C site

<400> 53  
 gatgtatgta ggggcggggt aagtaatgc

29

<210> 54  
 <211> 28  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Conserved portion of Zif268 protein

<400> 54

Gly	Glu	Lys	Pro	Phe	Ala	Cys	Asp	Ile	Cys	Gly	Arg	Lys	Phe	Ala	Arg
1				5				10					15		

Ser	Asp	Glu	Arg	Lys	Arg	His	Thr	Lys	Ile	His	Leu
			20					25			

<210> 55  
 <211> 41  
 <212> DNA  
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<220>

<223> EcoRIfootF primer

<400> 55  
 gaggaggagg aattccgaca ttataatga acgtgaattg c

41

<210> 56  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> C7-C73>5 primer

<400> 56  
 tgcgcccacg ccgcccacgc gatgattggg agcttttttt gcacg

45

<210> 57  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> C7-C75>3 primer

<400> 57

tcgcgtgggc ggcgtgggcg caaaaaatta ttatcatgga ttctaaaacg g

51

<210> 58

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> NotIfootB primer

<400> 58

gaggaggagg cggccgcagg tagatgagat gtgacgaacg tg

42

<210> 59

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Sp1C-C73>5 primer

<400> 59

tgccccgcc cgcgccacgc gatgattggg agcttttttt gcacg

45

<210> 60

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Sp1C75>3 primer

<400> 60

tcgcgtgggc gggggcgggg caaaaaatta ttatcatgga ttctaaaacg g

51

<210> 61

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence of six finger protein C7-C7

<400> 61

gcgtgggcgg cgtgggcg

18

<210> 62

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence of six-finger protein Sp1C-C7

<400> 62  
gcgtgggcgg gggcgggg 18

<210> 63  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Altered zif268 finger 1 binding site

<400> 63  
cctgcgtggt gtcccttttg ggacacaacg cagg 34

<210> 64  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Altered zif268 finger 2 binding site

<400> 64  
cctgcgttgg cgcccttttg ggcgccaacg cagg 34

<210> 65  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Altered zif268 finger 3 binding site

<400> 65  
cctctgtggg cgcccttttg ggcgcccaca gagg 34

<210> 66  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Linker peptide

<400> 66

Thr Gly Gln Lys Pro  
1 5

<210> 67  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Linker peptide

<400> 67

Thr Gly Glu Lys Pro  
1 5

<210> 68

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> (GCG)6 probe

<400> 68

gcggcggcgg cggcggcg

18

<210> 69

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> SV40 large T antigen

<400> 69

Pro Lys Lys Arg Lys Val  
1 5

<210> 70

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved portion of Zif268 protein

<400> 70

Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg  
1 5 10 15

Ser Asp His Leu Thr Thr His Ile Arg Thr His Thr  
20 25

<210> 71

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of zif268 sequence

<400> 71

tgcgcccacg ccgcccacgc ga

22

<210> 72

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of zif268 sequence

<400> 72

tgccccgccc ccgcccacgc ga

22

<210> 73

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 1 of zif268

<400> 73

Arg Asp Glu Leu Thr Arg

1 5

<210> 74

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 1 of zif268

<400> 74

Lys Ala Asp Leu Lys Arg

1 5

<210> 75

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 1 of zif268

<400> 75

Lys Cys Val Arg Gly Arg

1 5

<210> 76

<211> 6

<212> PRT

<213> Artificial sequence



<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 76

Lys Cys Asp Arg Gly Arg  
 1 5

<210> 77  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 77

Lys Tyr Cys Arg Thr Arg  
 1 5

<210> 78  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 78

Lys Gln Leu Pro Trp Thr  
 1 5

<210> 79  
 <211> 6  
 <212> PRT  
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<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 79

Lys Asn Ser Gln His Pro  
 1 5

<210> 80  
 <211> 6  
 <212> PRT  
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<220>  
 <223> Modified sequence of finger 1 of zif268

<400> 80

Lys Cys Gln Met Asp Ser  
1 5

<210> 81  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 81

Gln Gln Val Thr Arg Thr  
1 5

<210> 82  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 82

Thr Gln Ser Gln Ser Pro  
1 5

<210> 83  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 83

Val His Ile Gln Ala Asn  
1 5

<210> 84  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 84

Gln Thr Ala Ser Lys Ala  
1 5

<210> 85  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 85

Pro Thr His Leu Gln Thr  
1 5

<210> 86  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 86

Pro Glu Arg Thr Gln Pro  
1 5

<210> 87  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 87

Thr Ser Glu Ala Asp His  
1 5

<210> 88  
<211> 6  
<212> PRT  
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<220>  
<223> Modified sequence of finger 1 of zif268

<400> 88

Ser Glu Gln Arg Tyr Pro  
1 5

<210> 89  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 89

His Gln Gln Asn Lys Pro  
1 5

<210> 90  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 90

Arg Gly Gln Gly Met Ala  
1 5

<210> 91  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 91

Arg Ala Arg Gln Thr Gly  
1 5

<210> 92  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 92

Glu Asn Ser Phe Thr Asp  
1 5

<210> 93  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 93

Asn Val Met Gly His Asp  
1 5

<210> 94  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 94

Asn Arg Gly Gln Arg Lys  
1 5

<210> 95  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 95

Ser Arg Pro Ser Gln Trp  
1 5

<210> 96  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 1 of zif268

<400> 96

Thr Ser Glu Ala Asp His  
1 5

<210> 97  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Modified sequence of finger 2 of zif268

<400> 97

Thr Tyr Leu Asn Thr Pro  
1 5

<210> 98

<211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 98

Gly Tyr Arg Ala Ala Pro  
 1 5

<210> 99  
 <211> 6  
 <212> PRT  
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<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 99

Leu Tyr Arg Tyr His Leu  
 1 5

<210> 100  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 100

Pro Thr Leu Val Asn Ala  
 1 5

<210> 101  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 101

Val Arg Pro His Gln Arg  
 1 5

<210> 102  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 102

Pro Phe Cys Pro Tyr Arg  
1 5

<210> 103

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 103

Gly Val Thr Met Gln Pro  
1 5

<210> 104

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 104

Pro Gln Pro Leu Ser Asp  
1 5

<210> 105

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 105

Arg Glu Gln Val Ser Arg  
1 5

<210> 106

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 106

Thr His Met Trp Met Ile

1

5

<210> 107  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 107

Gln Arg Met Arg Thr Leu  
 1 5

<210> 108  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 108

Gln Arg Val Gly Leu Phe  
 1 5

<210> 109  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 109

Leu Arg Thr Gly Asn Tyr  
 1 5

<210> 110  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 110

Glu Arg Glu Phe Ser Leu  
 1 5

<210> 111  
 <211> 6



<212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 111

Glu Lys Glu Ser Arg Gly  
 1 5

<210> 112  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 112

Glu Gly Val Arg Lys Asn  
 1 5

<210> 113  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 113

Thr Gly Val Asn Ser Ile  
 1 5

<210> 114  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 2 of zif268

<400> 114

Thr Gln Ala Arg Pro Pro  
 1 5

<210> 115  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Modified sequence of finger 3 of zif268

<400> 115

Arg Asp Glu Arg Lys Arg  
1 5

<210> 116

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 116

Arg Asp Leu Ala Asn Ser  
1 5

<210> 117

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 117

Ser Gly Gln Trp Trp Arg  
1 5

<210> 118

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 118

Ser Leu Leu Val Ile Ala  
1 5

<210> 119

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 119

Val Ser Val Arg Gly Leu  
1 5

<210> 120  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Modified sequence of finger 3 of zif268  
  
 <400> 120

Asn Val Gly Asp Lys Pro  
 1 5

<210> 121  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Modified sequence of finger 3 of zif268  
  
 <400> 121

Ser Trp Ile Cys Gly Ile  
 1 5

<210> 122  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Modified sequence of finger 3 of zif268  
  
 <400> 122

Ile Ala Trp Met Glu Leu  
 1 5

<210> 123  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Modified sequence of finger 3 of zif268  
  
 <400> 123

Ile Met Met Thr Phe Phe  
 1 5

<210> 124  
 <211> 6  
 <212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 124

Arg Glu Cys Arg Met Leu

1 5

<210> 125

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 125

Ile Ala Leu Leu Asp Thr

1 5

<210> 126

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 126

Asn Val Gln Gly Leu Arg

1 5

<210> 127

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved portion of Zif268 protein

<400> 127

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg

1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr

20 25 30

F9  
cont